

SEQUENCE LISTING

<110> Bruce, Wesley B.

<120> A Nitrate-Responsive Root  
Transcriptional Factor

<130> 1263

<150> US 60/238,292

<151> 2000-10-05

<160> 2

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1280

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (360) ... (1082)

<400> 1

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tcctcccttg	ggaaacacctgc	tgccttttag	ctttcttctt	cgagagctcc	caccagatct	180
cctcctccctt	accttcttgc	gcacgttccgg	cggcgccgcgc	ggagaaaagat	agatcccccc	240
atcgctgtcg	tcggtccttg	cttccgatcg	gagggccaca	accacaacct	ctcgctccat	300
agcgtgcaag	cgcgagccag	ggtcaagaag	agagctagct	agctataaggc	cgaggatcg	359
atg ggg	agg gga	aag atc	gtg atc	cgc agg	atc gat	407
Met Gly Arg	Gly Lys Ile	Val Ile Arg	Arg Ile Asp	Asn Ser Thr	Ser	
1	5	10	15			
cg	cag	gtg	acc	tcc	aag	455
Arg	Gln	Val	Thr	Phe	Ser	Lys
20	25	30				
aag	gag	ctc	gcc	atc	ctc	503
Lys	Glu	Ile	Leu	Cys	Asp	Ala
35	40	45				
tcc	agc	acc	ggc	cgc	ctc	551
Ser	Ser	Thr	Gly	Arg	Leu	Tyr
50	55	60				
gtt	ata	gat	cg	tg	aa	599
Val	Ile	Asp	Arg	Tyr	Gly	Lys
65	70	75	80			
aat	ccc	aac	tcg	gag	ctt	647
Asn	Pro	Asn	Ser	Glu	Leu	Lys
85	90	95				

Zea mays L.

aga caa caa ctg cac aac ttg caa gaa aat tat	cgg cag ttg acg gga	695	
Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr	Arg Gln Leu Thr Gly		
100	105	110	
gat gat ctt tct ggg ctg aat gtc aaa gaa ctg cag	tcc ctg gag aat	743	
Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln	Ser Leu Glu Asn		
115	120	125	
caa ttg gaa aca agc ctg cgt ggt gtc cgc gca aag	aag gac cat ctc	791	
Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala	Lys Lys Asp His Leu		
130	135	140	
ttg ata gat gag att cac gat ttg aat cga aag	gca agt tta ttt cac	839	
Leu Ile Asp Glu Ile His Asp Leu Asn Arg	Lys Ala Ser Leu Phe His		
145	150	155	160
caa gaa aat aca gac ttg tac aat aag atc aac	ctg att cgc caa gaa	887	
Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn	Leu Ile Arg Gln Glu		
165	170	175	
aat gat gag tta cat aaa aag ata tat gag act	gaa gga cca agt gga	935	
Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr	Gly Pro Ser Gly		
180	185	190	
gtt aat cg <sup>g</sup> gag tca cc <sup>g</sup> act cca tt <sup>c</sup> aac tt <sup>t</sup> gca gta gta gaa acc	acc	983	
Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe	Ala Val Val Glu Thr		
195	200	205	
aga gat gtt cct gtg caa ctt gaa ctc agc aca	ctg cca cag caa aat	1031	
Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr	Leu Pro Gln Gln Asn		
210	215	220	
aac att gag cca tct act gct cct aag cta gga	ttg caa tta att cca	1079	
Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly	Leu Gln Leu Ile Pro		
225	230	235	240
tga agaagagtaa aactgccgtc ttatgatgct gaaggaaact	atttatttgt	1132	
*			
aagagatgat actcagagaa agacatattt gtggcagggaa	gatttgagat atgaacttat	1192	
aatgtatg caaataattt tcagaccgga atggggtcgt	ggaattcaga ggatgattgc	1252	
tttctaaaaa aaaaaaaaaa aaaaaaaaaa		1280	
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<211> 240			
<212> PRT			
<213> Zea mays			
<400> 2			
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1 5 10 15			
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala			
20 25 30			
Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Val Ile Phe			
35 40 45			
Ser Ser Thr Gly Arg Leu Tyr Glu Tyr Ser Ser Thr Ser Met Lys Ser			

50	55	60
Val Ile Asp Arg Tyr Gly Lys Ala Lys Glu Glu Gln Gln Val Val Ala		
65	70	75
Asn Pro Asn Ser Glu Leu Lys Phe Trp Gln Arg Glu Ala Ala Ser Leu		80
85	90	95
Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly		
100	105	110
Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn		
115	120	125
Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys Asp His Leu		
130	135	140
Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser Leu Phe His		
145	150	155
Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile Arg Gln Glu		160
165	170	175
Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly Pro Ser Gly		
180	185	190
Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val Val Glu Thr		
195	200	205
Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro Gln Gln Asn		
210	215	220
Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln Leu Ile Pro		
225	230	235
		240